Towards identifying the dynamic cellular patterns underlying early *Arabidopsis* floral development.

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A major challenge in developmental biology is to understand how multicellular tissues are organised into complex shapes. The various genetic, hormonal and mechanical events that drive morphogenesis must act by altering the properties of groups of cells in a coordinated manner through time and space. To gain a clear understanding of these events, we generate digital reconstructions of growing *Arabidopsis* flowers, and use these to precisely quantify cellular properties during the early stages of flower development. Our goal is to then analyse these data with the appropriate mathematical methodology, in order to determine precisely which cellular properties (and in what measure) best characterises the emerging differentiation states that are essential to morphogenesis.
We propose to identify and characterize cellular patterns based on measured cellular properties, linking their spatio-temporal behaviour to the observed changes induced by organogenesis.

Our experiments begin with imaging the flower from multiple angles. These images are then fused to generate a high-resolution reconstruction, which is then segmented. By imaging the same flower bud over several days and by identifying cell lineages between time points, we generate 4-D data on the development of the flower. From these data, several spatial and spatio-temporal cell properties like volume, volumetric growth or strain were extracted. We have adopted a graph-based approach to organise the data. The 3D tissue observed at successive dates/time points is transformed into a graph whose vertices represent cells and edges represent either cell spatial neighborhood or temporal relations between cells based on lineage. This graph thus contains all the spatio-temporal information about the flower under study. While developing the methods to analyse these growing tissues, we have opted to initially simplify the task in two ways, by restricting the study to the earliest morphogenetic events in the flower (stages 1-3), and by examining only the outermost cell layer, the L1.

This rich spatio-temporal information is used in two ways to study the events underlying flower development. Firstly, we applied a supervised approach to explore the properties of specific groups of cells, identified either by morphology or by gene expression. Secondly, we applied an unsupervised approach to identify cellular patterns. More specifically, a clustering method was applied to all the cells of one (or several) observed tissue sequence in order to identify homogeneous regions corresponding to specific cell behaviours.

One important long-term goal is to determine how these cellular patterns diverge in mutants presenting a different phenotype, and to identify shifts or changes in properties within these groups or the presence or absence of certain groups. I will detail my approach and present preliminary results of my analyses.